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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=5; day=1; hr=15; min=18; sec=40; ms=565; ]

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\*\*\*\*\*

Reviewer Comments:

<210> 40

<211> 374

<212> PRT

<213> *Pichia pastoris*

<220>

<221> MOD\_RES

<222> (176)...(190)

<223> Variable amino acid

<220>

<221> MOD\_RES

<222> (202)...(213)

<223> Variable amino acid

<400> 40

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Ile	Arg	Gln	Gly	Glu	Leu	Asp	Tyr	Ser	Asn	Ile	Phe	Gly	Asp	Thr	Gly
			20					25					30		
Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	His	Ala	Tyr	Ser	Val	Leu	Ser
			35				40						45		
Trp	Tyr	Ser	Asp	Gly	Gly	Glu	Asp	Val	Ser	Phe	Val	Gln	Gln	Ala	Phe
	50				55					60					
Gly	Trp	Leu	Tyr	Leu	Gly	Cys	Leu	Leu	Leu	Ser	Ile	Ser	Ser	Tyr	Phe
65				70					75					80	
Phe	Ser	Gly	Leu	Gly	Lys	Ile	Pro	Pro	Val	Tyr	Phe	Val	Leu	Leu	Val
			85					90					95		
Ala	Ser	Lys	Arg	Leu	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn	Asp

				100					105					110			
Cys	Leu	Thr	Thr	Phe	Leu	Met	Leu	Ala	Thr	Ile	Ile	Ile	Leu	Gln	Gln		
				115					120					125			
Ala	Ser	Ser	Trp	Arg	Lys	Asp	Gly	Thr	Thr	Ile	Pro	Leu	Ser	Val	Pro		
				130					135					140			
Asp	Ala	Ala	Asp	Thr	Tyr	Ser	Leu	Ala	Ile	Ser	Val	Lys	Met	Asn	Xaa		
145					150					155					160		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp	
				165					170					175			
Glu	Asn	Leu	Ile	Lys	Ala	Leu	Ala	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
				180					185					190			
Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Ser	Phe	Ile	Leu	Pro	Leu	His	Tyr	Asp	Asp		
				195					200					205			
Gln	Ala	Asn	Glu	Ile	Arg	Ser	Ala	Tyr	Phe	Arg	Gln	Ala	Phe	Asp	Phe		
				210					215					220			
Ser	Arg	Gln	Phe	Leu	Tyr	Lys	Trp	Thr	Val	Asn	Trp	Arg	Phe	Leu	Ser		
225					230					235					240		
Gln	Glu	Thr	Phe	Asn	Asn	Val	His	Phe	His	Gln	Leu	Leu	Phe	Ala	Leu		
				245					250					255			
His	Ile	Ile	Thr	Leu	Val	Leu	Phe	Ile	Leu	Lys	Phe	Leu	Ser	Pro	Lys		
				260					265					270			
Asn	Ile	Gly	Lys	Pro	Leu	Gly	Arg	Phe	Val	Leu	Asp	Ile	Phe	Lys	Phe		
				275					280					285			
Trp	Lys	Pro	Thr	Leu	Ser	Pro	Thr	Asn	Ile	Ile	Asn	Asp	Pro	Glu	Arg		
				290					295					300			
Ser	Pro	Asp	Phe	Val	Tyr	Thr	Val	Met	Ala	Thr	Thr	Asn	Leu	Ile	Gly		
305					310					315					320		
Val	Leu	Phe	Ala	Arg	Ser	Leu	His	Tyr	Gln	Phe	Leu	Ser	Trp	Tyr	Ala		
				325					330					335			
Phe	Ser	Leu	Pro	Tyr	Leu	Leu	Tyr	Lys	Ala	Arg	Leu	Asn	Phe	Ile	Ala		
				340					345					350			
Ser	Ile	Ile	Val	Tyr	Ala	Ala	His	Glu	Tyr	Cys	Trp	Leu	Val	Phe	Pro		
				355					360					365			
Ala	Thr	Glu	Gln	Ser	Ser												
				370													

The above <222> responses describing Xaa locations are incorrect: Xaa is located at positions 160-174 and 186-197, not at locations 202-213.

\*\*\*\*\*

Application No: 10500240

Version No: 3.0

**Input Set:****Output Set:****Started:** 2008-04-15 16:02:05.595**Finished:** 2008-04-15 16:02:13.772**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 177 ms**Total Warnings:** 33**Total Errors:** 53**No. of SeqIDs Defined:** 106**Actual SeqID Count:** 106

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)

**Input Set:**

**Output Set:**

**Started:** 2008-04-15 16:02:05.595  
**Finished:** 2008-04-15 16:02:13.772  
**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 177 ms  
**Total Warnings:** 33  
**Total Errors:** 53  
**No. of SeqIDs Defined:** 106  
**Actual SeqID Count:** 106

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (24)
E 257	Invalid sequence data feature in <221> in SEQ ID (26)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (36)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (38)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 257	Invalid sequence data feature in <221> in SEQ ID (40)
E 341	'Xaa' position not defined SEQID (40) POS (160)
E 341	'Xaa' position not defined SEQID (40) POS (161)
E 341	'Xaa' position not defined SEQID (40) POS (162)
E 341	'Xaa' position not defined SEQID (40) POS (163)
E 341	'Xaa' position not defined SEQID (40) POS (164)
E 341	'Xaa' position not defined SEQID (40) POS (165)
E 341	'Xaa' position not defined SEQID (40) POS (166)
E 341	'Xaa' position not defined SEQID (40) POS (167)
E 341	'Xaa' position not defined SEQID (40) POS (168)
E 341	'Xaa' position not defined SEQID (40) POS (169)
E 341	'Xaa' position not defined SEQID (40) POS (170)
E 341	'Xaa' position not defined SEQID (40) POS (171)

**Input Set:**

**Output Set:**

**Started:** 2008-04-15 16:02:05.595  
**Finished:** 2008-04-15 16:02:13.772  
**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 177 ms  
**Total Warnings:** 33  
**Total Errors:** 53  
**No. of SeqIDs Defined:** 106  
**Actual SeqID Count:** 106

Error code	Error Description
E 341	'Xaa' position not defined SEQID (40) POS (172)
E 341	'Xaa' position not defined SEQID (40) POS (173)
E 341	'Xaa' position not defined SEQID (40) POS (174)
E 341	'Xaa' position not defined SEQID (40) POS (191)
E 341	'Xaa' position not defined SEQID (40) POS (192)
E 341	'Xaa' position not defined SEQID (40) POS (193)
E 341	'Xaa' position not defined SEQID (40) POS (194)
E 341	'Xaa' position not defined SEQID (40) POS (195) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
E 257	Invalid sequence data feature in <221> in SEQ ID (42)
W 402	Undefined organism found in <213> in SEQ ID (44)
W 402	Undefined organism found in <213> in SEQ ID (45)
W 402	Undefined organism found in <213> in SEQ ID (46)
W 402	Undefined organism found in <213> in SEQ ID (48)
E 257	Invalid sequence data feature in <221> in SEQ ID (54)
E 257	Invalid sequence data feature in <221> in SEQ ID (56)
E 257	Invalid sequence data feature in <221> in SEQ ID (58)
E 257	Invalid sequence data feature in <221> in SEQ ID (60)
E 257	Invalid sequence data feature in <221> in SEQ ID (62)
E 257	Invalid sequence data feature in <221> in SEQ ID (68)
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**Input Set:**

**Output Set:**

**Started:** 2008-04-15 16:02:05.595  
**Finished:** 2008-04-15 16:02:13.772  
**Elapsed:** 0 hr(s) 0 min(s) 8 sec(s) 177 ms  
**Total Warnings:** 33  
**Total Errors:** 53  
**No. of SeqIDs Defined:** 106  
**Actual SeqID Count:** 106

Error code	Error Description
E 257	Invalid sequence data feature in <221> in SEQ ID (78) This error has occurred more than 20 times, will not be displayed
W 402	Undefined organism found in <213> in SEQ ID (86)
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W 402	Undefined organism found in <213> in SEQ ID (88)
W 402	Undefined organism found in <213> in SEQ ID (90)
W 402	Undefined organism found in <213> in SEQ ID (92)
W 402	Undefined organism found in <213> in SEQ ID (94)

# SEQUENCE LISTING

<110> WILDT, Stefan  
 MIELE, Robert G.  
 NETT, Juergen H.  
 DAVIDSON, Robert C.

<120> METHODS TO ENGINEER MAMMALIAN-TYPE  
 CARBOHYDRATE STRUCTURES

<130> GF0022P

<140> 10500240

<141> 2005-03-23

<150> PCT/US02/41510

<151> 2002-12-24

<150> 60/344,169

<151> 2001-12-27

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<210> 1

<211> 35

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<213> Artificial Sequence

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<223> Primer

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<223> Primer

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<212> DNA

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ccatccagtg tcgaaaacga gccaatgggt catgtctata aatc 44

<210> 10

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<400> 10

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<210> 11

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<220>

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 <400> 18  
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<220>  
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<210> 20  
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<220>  
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<220>  
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<400> 21  
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<220>  
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<400> 22  
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<400> 23  
His Asp Glu Leu  
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<210> 24  
<211> 458  
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<222> (304)...(318)  
<223> Variable amino acid

<220>  
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<222> (416)...(436)  
<223> Variable amino acid

<400> 24

Met	Glu	Gly	Glu	Gln	Ser	Pro	Gln	Gly	Glu	Lys	Ser	Leu	Gln	Arg	Lys
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Gln	Phe	Val	Arg	Pro	Pro	Leu	Asp	Leu	Trp	Gln	Asp	Leu	Lys	Asp	Gly
			20					25					30		
Val	Arg	Tyr	Val	Ile	Phe	Asp	Cys	Arg	Ala	Asn	Leu	Ile	Val	Met	Pro
			35				40					45			
Leu	Leu	Ile	Leu	Phe	Glu	Ser	Met	Leu	Cys	Lys	Ile	Ile	Ile	Lys	Lys
			50				55				60				
Val	Ala	Tyr	Thr	Glu	Ile	Asp	Tyr	Lys	Ala	Tyr	Met	Glu	Gln	Ile	Glu
65					70				75					80	
Met	Ile	Gln	Leu	Asp	Gly	Met	Leu	Asp	Tyr	Ser	Gln	Val	Ser	Gly	Gly
				85					90					95	
Thr	Gly	Pro	Leu	Val	Tyr	Pro	Ala	Gly	His	Val	Leu	Ile	Tyr	Lys	Met
			100					105					110		
Met	Tyr	Trp	Leu	Thr	Glu	Gly	Met	Asp	His	Val	Glu	Arg	Gly	Gln	Val
			115				120					125			
Phe	Phe	Arg	Tyr	Leu	Tyr	Leu	Leu	Thr	Leu	Ala	Leu	Gln	Met	Ala	Cys
			130				135					140			
Tyr	Tyr	Leu	Leu	His	Leu	Pro	Pro	Trp	Cys	Val	Val	Leu	Ala	Cys	Leu
145					150					155				160	
Ser	Lys	Arg	Leu	His	Ser	Ile	Tyr	Val	Leu	Arg	Leu	Phe	Asn	Asp	Cys
				165					170					175	
Phe	Thr	Thr	Leu	Phe	Met	Val	Val	Thr	Val	Leu	Gly	Ala	Ile	Val	Ala
			180					185						190	
Ser	Arg	Cys	His	Gln	Arg	Pro	Lys	Leu	Lys	Lys	Ser	Leu	Ala	Leu	Val
			195				200					205			
Ile	Ser	Ala	Thr	Tyr	Ser	Met	Ala	Val	Ser	Ile	Lys	Met	Asn	Ala	Leu
			210				215					220			
Leu	Tyr	Phe	Pro	Ala	Met	Met	Ile	Ser	Leu	Phe	Ile	Leu	Asn	Asp	Ala
225					230					235				240	
Asn	Val	Ile	Leu	Thr	Leu	Leu	Asp	Leu	Val	Ala	Met	Ile	Ala	Trp	Gln
				245					250					255	
Val	Ala	Val	Ala	Val	Pro	Phe	Leu	Arg	Ser	Phe	Pro	Gln	Gln	Tyr	Leu
			260					265						270	
His	Cys	Ala	Phe	Asn	Phe	Gly	Arg	Lys	Phe	Met	Tyr	Gln	Trp	Ser	Ile
			275					280					285		
Asn	Trp	Gln	Met	Met	Asp	Glu	Glu	Ala	Phe	Asn	Asp	Lys	Arg	Phe	Xaa
			290				295					300			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Val
305					310					315				320	
Thr	Arg	Tyr	Pro	Arg	Ile	Leu	Pro	Asp	Leu	Trp	Ser	Ser	Leu	Cys	His
				325					330					335	
Pro	Leu	Arg	Lys	Asn	Ala	Val	Leu	Asn	Ala	Asn	Pro	Ala	Lys	Thr	Ile
			340					345					350		
Pro	Phe	Val	Leu	Ile	Ala	Ser	Asn	Phe	Ile	Gly	Val	Leu	Phe	Ser	Arg
			355				360						365		

Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile  
 370 375 380  
 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr  
 385 390 395 400  
 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Xaa  
 405 410 415  
 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
 420 425 430  
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 435 440 445  
 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn  
 450 455

<210> 25

<211> 458

<212> PRT

<213> *Saccharomyces cerevisiae*

<400> 25

Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys  
 1 5 10 15  
 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly  
 20 25 30  
 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro  
 35 40 45  
 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys  
 50 55 60  
 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu  
 65 70 75 80  
 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly  
 85 90 95  
 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met  
 100 105 110  
 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val  
 115 120 125  
 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys  
 130 135 140  
 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu  
 145 150 155 160  
 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys  
 165 170 175  
 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala  
 180 185 190  
 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val  
 195 200 205  
 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu  
 210 215 220  
 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala  
 225 230 235 240  
 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln  
 245 250 255  
 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu  
 260 265 270  
 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile  
 275 280 285  
 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His

290                      295                      300  
 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val  
 305                      310                      315                      320  
 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His  
                     325                      330                      335  
 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile  
                     340                      345                      350  
 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg  
                     355                      360                      365  
 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile  
                     370                      375                      380  
 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr  
 385                      390                      395                      400  
 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala  
                     405                      410                      415  
 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala  
                     420                      425                      430  
 Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg  
                     435                      440                      445  
 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn  
                     450                      455

<210> 26

<211> 443

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> MOD\_RES

<222> (333)...(347)

<223> Variable amino acid

<400> 26

Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg  
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 Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu  
                     20                      25                      30  
 Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys  
                     35                      40                      45  
 Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp  
                     50                      55                      60  
 Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly  
 65                      70                      75                      80  
 His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp  
                     85                      90                      95  
 His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr  
                     100                      105                      110  
 Leu Ala Leu Gln Met Ala Cys Tyr Tyr Leu Leu His Leu Pro Pro Trp  
                     115                      120                      125  
 Cys Val Val Leu Ala Cys Leu Ser Lys Arg Leu His Ser Ile Tyr Val  
                     130                      135                      140  
 Leu Arg Leu Phe Asn Asp Cys Phe Thr Thr Leu Phe Met Val Val Thr  
 145                      150                      155                      160  
 Val Leu Gly Ala Ile Val Ala Ser Arg Cys His Gln Arg Pro Lys Leu  
                     165                      170                      175  
 Lys Lys His Gln Thr Cys Lys Val Pro Pro Phe Val Phe Phe Phe Met

180	185	190
Cys Cys Ala Ser Tyr Arg Val	His Ser Ile Phe Val	Leu Arg Leu Phe
195	200	205
Asn Asp Pro Val Ala Met Val	Leu Leu Phe Leu Ser	Ile Asn Leu Leu
210	215	220
Leu Ala Gln Arg Trp Gly Trp	Gly Ser Leu Ala Leu	Val Ile Ser Ala
225	230	235
Thr Tyr Ser Met Ala Val Ser	Ile Lys Met Asn Ala	Leu Leu Tyr Phe
245	250	255
Pro Ala Met Met Ile Ser Leu	Phe Ile Leu Asn Asp	Ala Asn Val Ile
260	265	270
Leu Thr Leu Leu Asp Leu Val	Ala Met Ile Ala Trp	Gln Val Ala Val
275	280	285
Ala Val Pro Phe Leu Arg Ser	Phe Pro Gln Gln Tyr	Leu His Cys Ala
290	295	300
Phe Asn Phe Gly Arg Lys Phe	Met Tyr Gln Trp Ser	Ile Asn Trp Gln
305	310	315
Met Met Asp Glu Glu Ala Phe	Asn Asp Lys Arg Phe	Xaa Xaa Xaa Xaa
325	330	335
Xaa Xaa Xaa Xaa Xaa Xaa Xaa	Xaa Xaa Xaa Xaa Phe	Val Thr Arg Tyr
340	345	350
Pro Arg Ile Leu Pro Asp Leu	Trp Ser Ser Leu Cys	His Pro Leu Arg
355	360	365
Lys Asn Ala Val Leu Asn Ala	Asn Pro Ala Lys Thr	Ile Pro Phe Val
370	375	380
Leu Ile Ala Ser Asn Phe Ile	Gly Val Leu Phe Ser	Arg Ser Leu His
385	390	395
Tyr Gln Phe Leu Ser Trp Tyr	His Trp Thr Leu Pro	Ile Leu Ile Phe
405	410	415
Trp Ser Gly Met Pro Phe Phe	Val Gly Pro Ile Trp	Tyr Val Leu His
420	425	430
Glu Trp Cys Trp Asn Ser Tyr	Pro Pro Asn Ser	
435	440	

<210> 27

<211> 373

<212> PRT

<213> Homo sapiens

<400> 27

Trp Gln Glu Arg Arg Leu Leu	Leu Arg Glu Pro Arg Tyr Thr	Leu Leu
1	5	10
Val Ala Ala Cys Leu Cys Leu	Ala Glu Val Gly Ile Thr Phe	Trp Val
20	25	30
Ile His Arg Val Ala Tyr Thr	Glu Ile Asp Trp Lys Ala Tyr	Met Ala
35	40	45
Glu Val Glu Gly Val Gly Thr	Tyr Asp Tyr Thr Gln Leu Gln	Gly Asp
50	55	60
Thr Gly Pro Leu Val Tyr Pro	Ala Gly Phe Val Tyr Ile Phe	Met Gly
65	70	75
Leu Tyr Tyr Ala Thr Ser Arg	Gly Thr Asp Ile Arg Met Ala	Gln Asn
85	90	95
Ile Phe Ala Val Leu Tyr Leu	Ala Thr Leu Leu Leu Val Phe	Leu Ile
100	105	110
Tyr His Gln Thr Cys Lys Val	Pro Pro Phe Val Phe Phe	Phe Met Cys
115	120	125

Cys	Ala	Ser	Tyr	Arg	Val	His	Ser	Ile	Phe	Val	Leu	Arg	Leu	Phe	Asn		
130						135				140							
Asp	Pro	Val	Ala	Met	Val	Leu	Leu	Phe	Leu	Ser	Ile	Asn	Leu	Leu	Leu		
145						150				155						160	
Ala	Gln	Arg	Trp	Gly	Trp	Gly	Cys	Cys	Phe	Phe	Ser	Leu	Ala	Val	Ser		
165						170				175							
Val	Lys	Met	Asn	Val	Leu	Leu	Phe	Ala	Pro	Gly	Leu	Leu	Phe	Leu	Leu		
180						185				190							
Leu	Thr	Gln	Phe	Gly	Phe	Arg	Gly	Ala	Leu	Pro	Lys	Leu	Gly	Ile	Cys		
195						200				205							
Ala	Gly	Leu	Gln	Val	Val	Leu	Gly	Leu	Pro	Phe	Leu	Leu	Glu	Asn	Pro		
210						215				220							
Ser	Gly	Tyr	Leu	Ser	Arg	Ser	Phe	Asp	Leu	Gly	Arg	Gln	Phe	Leu	Phe		
225						230				235						240	
His Trp Thr Val Asn																	